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 70 80 90 100 110 120
 TCTCTTCCTG GATCCTTCAG AGCTCTTGTC AATTCCTCAC GTTTTTTTTT GTTTTTTCGT
 130 140 150 160 170 180
 CGTTTAATTG TGGAAACACA TATCCGTCCT CTTTGAAACA GCATCAGAAA ACTTTCTGCT
 190 200 210 220 230 240
 CTCCTGTGCC TTCTACTTAC TCTGATTGCC TTAGTTAGTC ACATCGCAAG CAACA ACTAA
 250 260 270 280 290 300
 CTGCCAATGG GAGGAGCCAG TTGGAGCAGG GTGCGTGCTC GGTGCTCTTT TCAGAAGGTT
 310 320 330 340 350 360
 TTCTCTTG TG CCAGCATGCT TTTTGTAGGC TGTGTCATCA CAATGAACAT GTGTGAGTTC
 370 380 390 400 410 420
 ATCCGCTCTGG ATTATTCTTT TTCTTACGTC TTCTGAGTAC TTCATACTTT CCAAATTTTT
 430 440 450 460 470 480
 CAACTGA ACT TTTCTTCTTT TCTCATTGAA GTGGTTTGGT TTTGGTTCGCG TGATCAACGG
 490 500 510 520 530 540
 ATCCTACTTT TTTGAAACAA AATGTTTTTG AAGTTTCACA GACTGATTTC GGGGTTTTTT
 550 560 570 580 590 600
 CAAAGAATAT ATTCCCTCTC GAGCAAGAGA AAATCCAGA AAATAGTAGT TTTTTTCAAT
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 TAGTCGTTTC ATTTGTACTA GCTAAAAAC TTGCAACTTA TGGCTTTAAA ACATGTGTTG
 670 680 690 700 710 720
 GCTTCATACA AAAACATTTA ACTAGTGT TTCCAGTTTT GTGTTCGTTT CATTTTCTCA
 730 740 750 760 770 780
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 850 860 870 880 890 900
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 910 920 930 940 950 960
 AGGTGCCAAT GCGGTGAAAG AAAATTG A GTTTATTCC TGAAATCACA CTACTCTTGC
 970 980 990 1000 1010 1020
 TTTTATTTGT AACTCTACA CAGGTAGTT GGTGATTCT AGATCTCTTG CCTCCTAGCT
 1030 1040 1050 1060 1070 1080
 TGCAAGGATA ATATAATTGA ATTGTTTTTG AGGAGTGCAA AGATTGAATA GTTTTCTATA
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 1210 1220 1230 1240 1250 1260
 TTAATATTGA GATTCATGTA CAGGTTGGTA GACTCTATAA TTGCACACCA ATATGTGAAA
 1270 1280 1290 1300 1310 1320
 GTTTTCTTTA AAATTAAACT GCTGTAAATG ACTTTTGAAT AAGTTTATCA GATAGAAATT
 1330 1340 1350 1360 1370 1380
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 1390 1400 1410 1420 1430 1440
 ATTTATCTCT TTGCTACAAT TTCTCCACA AAGCCTTTTT CTTCATTAA CGTTCTTTTT
 1450 1460 1470 1480 1490 1500
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 TGAAAAATTA TTGGATTGGG AGTTGTGGGA GTGAAGAGAT GGGTCAAAAG CCATCAATCT
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 AAGTGAACA AGAAATTTGG AAAATAGAGA TACATATGTA TATGAAAATA GAATTGAACA
 2170 2180 2190 2200 2210 2220
 GGAACCTATT TTTATTTTCA GGATATGGGA AGCTTGAATG AAATATCATC CGACTTTGAA
 2230 2240 2250 2260 2270 2280
 ATTGACATTT TATTCATCA ACTGTGGCAT GACTCGGCAC TTTCTTTTGC TCATCTTCCG

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2350 2360 2370 2380 2390 2400
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 TGATTAATTC AAAACGAACA ACCGTCCATG CATCACCATC GGAAAATGTG ATGGTTATTC

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2830 2840 2850 2860 2870 2880
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 GGTACTGGGA TCAGTTTCAA GTTACTTTCA CTTTCAAACG ACGATATGGA TTCTATATTA

3190 3200 3210 3220 3230 3240
 TTCAAGCCTA TGTTCGAACA TATCTTACAA TCATTGTATC TTGGGTTTCA TTCTGCATGG

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 AACCAAAAGC TCTGCGGCA AGAACAACG TCGGAATCTC ATCTCTTCTA GCTCTTACTT

3310 3320 3330 3340 3350 3360
 TCCAGTTTGG AAATATTTTG AAAAATCTTC CAAGGGTTTC ATATGTGAAA GGTTTGTTTT

3370 3380 3390 3400 3410 3420
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 GTGGATGCTT GGATGCATAT CATTGTCTT CGGAACCATG GTAGAATTGG CATTGTGTTG
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 TTACATTTCC CGTTGTCAGA ACAGCGTAAG AAAGTGAGTT GGCATAAGAG TTTTCTCACG
 3550 3560 3570 3580 3590 3600
 TGGAGGGAAG TAATTAAATT TTGGGTGTCA TATGAAAATA TCAAAAACAA TATCAGGAAA
 3610 3620 3630 3640 3650 3660
 ,TTGAATTTCA CTATGATTTT GTAGTAAACA AATTACAGCG CGGAACGACG ACGGGAACGA
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 3730 3740 3750 3760 3770 3780
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4570 4580 4590 4600 4610 4620
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4630 4640 4650 4660 4670 4680
 TCTGTCTGAT CATGGTTTTT GGAAGTTATA TGTGAGCCAC

4690 4700 4710 4720 4730 4740
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 ACACCATGTT TATTGTAATT ACCAGGCTAC TATTTGCAGA TGCGATCAAC ATCACCACCT

4810 4820 4830 4840 4850 4860
 CCACCATCTG GATGTCTGGC CAGATTCAT CCGGAAGCAG TGGACAAATT CTCCATTGTA

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5050 5060 5070 5080 5090 5100
 GGTATCTACC TCCATTCTTT TCCGATGATT CGCAGTTTTT CACAGGGTTC AAATGTATCT

5110 5120 5130 5140 5150 5160
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5170 5180 5190 5200 5210 5220
 TTATGTACAT TGTGTTGGTA TTCAATTCGA AAAACAATGA AATTTATTTT TAAATAACTG

5230 5240 5250 5260 5270 5280
 CGTTTCTGGG GTTTCTATCA GCACTTACTA GCTGACAAAA ACTTTTCCGT ATTCGGAATT

5290 5300 5310 5320 5330 5340
 AGATTTTTAT GCAAGCAATG TTTCATTTTT ACACAGTATA GTATTTATTC TTACTTTTGA

5350 5360 5370 5380 5390 5400
 TTATATTGCT CGCACCTAA ATGACAGGTA TTAGAAATTA ACCGCTTTTC AGAGTATTTT

5410 5420 5430 5440 5450 5460
 TAATCTTCTT AGTACTAGTT TAGTTCTTTA AATAAGAAAC CATCTAGTTT TTCATTATCA

5470 5480 5490 5500 5510 5520
 CTCAACTTCA GTCGGACAAA TTTTAAATTT TTTACTCGAT AAAAAAATTT TATAATTCAG

5530 5540 5550
 ACAAATTATG TCTTCTCATT TTTGATCGCT

Fig. 1

20 30 40 50
 ATGAAGTTT TTCCTGAAAT CACACTACTC TTGCTTTTAT TGTACACTC
 60 70 80 90 100
 TACACAGGCT AAAGGAAAAC GACGGAAATG TCCGGAGGGT GCGTGGTCGG
 110 120 130 140 150
 AAGGAAAGAT TATGAACACG ATCATGAGCA ACTACACGAA AATGTTGCCC
 160 170 180 190 200
 GACGCGGAGG ACAGCGTACA AGTTAATATT GAGATTCATG TACAGGATAT
 210 220 230 240 250
 GGGAAGCTTG AATGAAATAT CATCCGACTT TGAAATTGAC ATTTTATTCA
 260 270 280 290 300
 CTCAACTGTG GCATGACTCG GCACTTTCCTT TTGCTCATCT TCCGGCTTGT
 310 320 330 340 350
 AAGCGAAATA TCACAATGGA AACACGACTT TTACCTAAGA TTTGGTCTCC
 360 370 380 390 400
 AAACACGTGT ATGATTAATT CAAAACGAAC AACCCTCCAT GCATCACCAT
 410 420 430 440 450
 CGGAAAATGT GATGGTTATT CTGTACGAGA ATGGAACAGT CTGGATTAAC
 460 470 480 490 500
 CATCGTCTTA GTGTCAAATC ACCTTGCAAT TTGGATCTGC GACAGTTTCC
 510 520 530 540 550
 TTTCGATACT CAAACTTGCA TATTAATCTT TGAATCCTAT AGTCATAACT
 560 570 580 590 600
 CAGAAGAAGT TGAACCTTCAT TGGATGGAAG AAGCTGTCAC ATTAATGAAG
 610 620 630 640 650
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 660 670 680 690 700
 AACTTTACTC TATCCAAACG GGTACTGGGA TCAGCTTCAA GTTACTTTCA
 710 720 730 740 750
 CTTTCAAACG ACGATATGGA TTCTATATTA TTCAAGCCTA TGTTCACA
 760 770 780 790 800
 TATCTTACAA TCATTGTATC TTGGGTTTCA TTCTGCATGG AACCAAAGC
 810 820 830 840 850
 TCTGCCGGCA AGAACAACCTG TCGGAATCTC ATCTCTTCTA GCTCTTACTT
 860 870 880 890 900
 TCCAGTTTGG AAATATTTTG AAAAATCTTC CAAGGGTTTC ATATGTGAAA
 910 920 930 940 950
 GCAATGGATG TGTGGATGCT TGGATGCATA TCATTTGTCT TCGGAACCAT

Fig. 2

970 980 990 1000
 GGTAGAA GCATTTGTTT GTTACATTTT CCGTTGTCA ACAGCGTAA
 1010 1020 1030 1040 1050
 GAAACGCGGA ACGACGACGG GAACGAATGA GAAATTCTCA GGTGTGGGCA
 1060 1070 1080 1090 1100
 AACGGATCGT GTAGAACTAG AAGCAACGGG TATGCAAACG GGGGATCTGT
 1110 1120 1130 1140 1150
 AATCTCACAT TATCATCCAA CAAGCAATGG AAATGGGAAT AATAATCGAC
 1160 1170 1180 1190 1200
 ATGATACACC TCAAGTTACT GGAAGAGGAT CACTTCATCG AAACGGGGCCA
 1210 1220 1230 1240 1250
 CCATCTCCAT TAAACCTTCA AATGACTACA TTTGATTCCG AGATCCCTCT
 1260 1270 1280 1290 1300
 GACTTTTGAT CAGCTGCCAG TTTCCATGGA ATCCGATAGA CCCCTGATTG
 1310 1320 1330 1340 1350
 AAGAGATGCG ATCAACATCA CCACCTCCAC CATCTGGATG TCTGGCCAGA
 1360 1370 1380 1390 1400
 TTCCATCCGG AAGCAGTGGA CAAATTCTCC ATTGTAGCTT TTCCATTGGC
 1410 1420 1430 1440 1450
 ATTTACAATG TTAAATCTTG TCTACTGGTG GCACTATTTG TCTCAAACCT
 1460 1470
 TCGATCAAAA CTATCAGTGA

Fig. 2
 Page 2

20	30	40	50
MKFIPEI	LLLFVHSTQA	KGKRRKCEG	AWSEGKIMN
60	70	80	90
DAEDSVQVNI	EIHVQDMGSL	NEISSDFEID	ILFTQLWHDS
110	120	130	140
KRNITMETRL	LPKIMSPNTC	MINSKRRTVH	ASPSENVMI
160	170	180	190
HRLSVKSPCN	LDLRQFPFDT	QTCILIFESY	SHNSEEVELH
210	220	230	240
PIQLPDMV	HYSTKETLL	YPNGYWDQLQ	VTFTFKRRYG
260	270	280	290
YLTIIVSWVS	FCMEPKALPA	RTTVGISSLL	ALTFQFGNIL
310	320	330	340
AMDVWMLGCI	SFVFGTMVEL	AFVCYISRCQ	NSVRNAERRR
360	370	380	390
NGSCRTRSNG	YANGGSVISH	YHPTSNGNGN	NNRHDTQPVT
410	420	430	440
PSPLNLQMTT	FDSEIPLTFD	QLPVSMESDR	PLIEEMRSTS
460	470	480	
FHPEAVDKFS	IVAFPLAFTM	FNLVYWWHYL	SQTFDQNYQ

Fig. 3

MOD-1 is similar
to ligand-gated ion channels

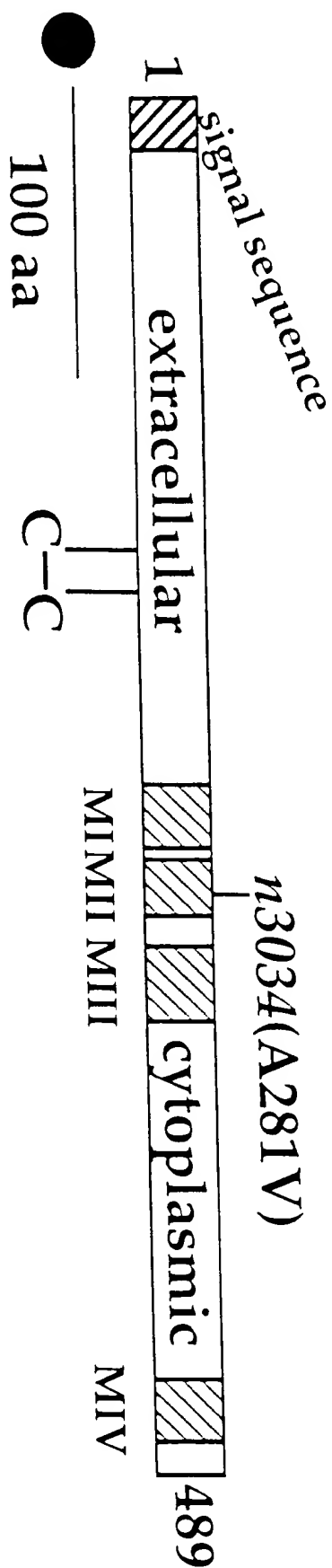


Fig. 4

ok103 is a 4135 bp deletion allele of *mod-1*

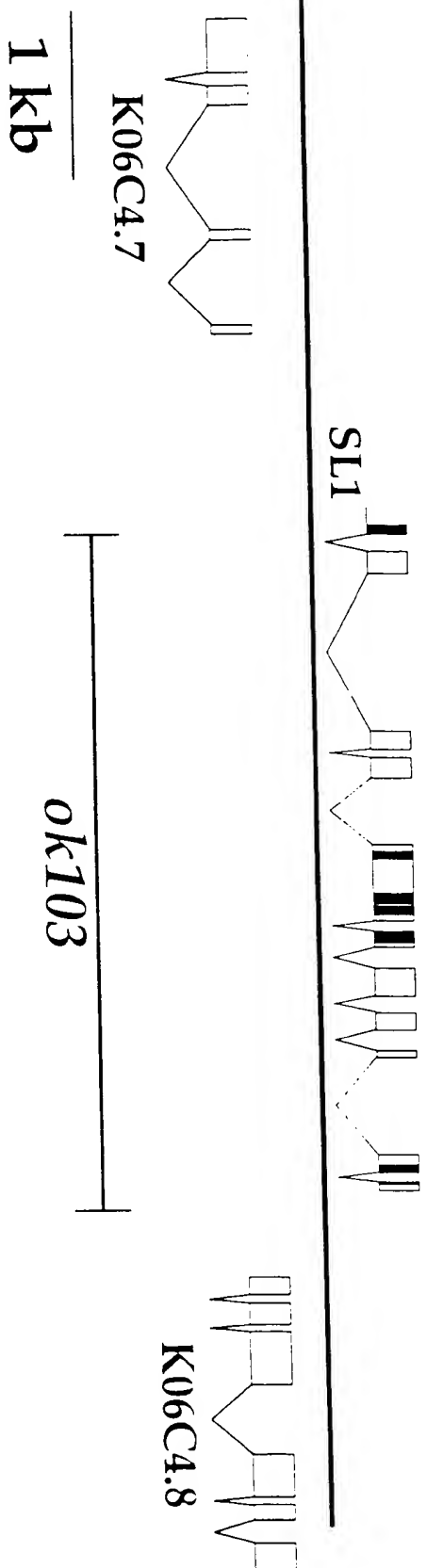


Fig. 5

20 30 40 50 60
 TCATGTTTCA CGGAACGACG AATTTATCCC GTCGTTTCTT CTTTCCGTT TTAACTCATA
 70 80 90 100 110 120
 TCTCTTCCTG GATCCTTCAG AGCTCTTGTC AATTCCTCAC GTTTTTTTTTT GTTTTTTCGT
 130 140 150 160 170 180
 CGTTTAATTG TGGAAACACA TATCCGTCCT CTTTGAAACA GCATCAGAAA ACTTTCGTCT
 190 200 210 220 230 240
 CTCCGTGTCC TTCTACTTAC TCTGATTGCC TTAGTTAGTC ACATCGCAAG CAACAACATA
 250 260 270 280 290 300
 CTGCCAATGG GAGGAGCCAG TTGGAGCAGG GTGCGTGCTC GGTGCTCTTT TCAGAAGGTT
 310 320 330 340 350 360
 TTCTCTGTG CCAGCATGCT TTTTGGAGGC TGTGTCATCA CAATGAACAT GTGTGAGTTC
 370 380 390 400 410 420
 ATCCGTCTGG ATTATTCTTT TTCTTACGTC TTCTGAGTAC TTCATACTTT CCAAATTTTT
 430 440 450 460 470 480
 CAACTGAAC TTTCTTCTTT TCTCATTGAA GTGGTTTGGT TTTGGTCGCG TGATCAACGG
 490 500 510 520 530 540
 ATCCTACTTT TTTGAAACAA AATGTTTTTG AAGTTTCACA GACTGATTTC GGGGTTTTTT
 550 560 570 580 590 600
 CAAAGAATAT ATTCCCTCTC GAGCAAGAGA AAATTCAGAA AAATAGTAGT TTTTTCATAT
 610 620 630 640 650 660
 TAGTCGTTTC ATTTGTACTA GCTAAAAAC TTGCAACTTA TGGCTTTAAA ACATGTGTG
 670 680 690 700 710 720
 GCTTCATACA AAAACATTTA ACTAGTGTTT TTCCAGTTTT GTGTTCGTTT CATTTTCTCA
 730 740 750 760 770 780
 CCAAACCTGAC AATAATTACT TTCTGTGAAC GTGTTTTGTA GGCAAGCTCC CGAATATTTT
 790 800 810 820 830 840
 TTTCTCTTCT CACGTCTTGT TATTTTCTCG ATTTTATTTT CTGAATCTGT GCGGTTTTCA
 850 860 870 880 890 900
 ATCAATTTGA TTGCGATAAT TATTCTATCA GAAATATATT TTCAGAAATC CAAATACTCC
 910 920 930 940 950 960
 AGGTGCCAAT GCGGTGAAAG AAAATTGTA AGTTTATTCC TGAAATCACA CTACTCTTGC
 970 980 990 1000 1010 1020
 TTTTATTTGT ACACTCTACA CAGGTTAGTT TCTCTTGAAT GTCCATTTTA ATATTTATAG
 1030 1040 1050 1060 1070 1080
 AACACTTTTA TGTACATTGT GTTGGTATTC AATTCGAAAA ACAATGAAAT TTATTTCTAA
 1090 1100 1110 1120 1130 1140
 ATAAC TGCGT TTCTGGGGTT TCTATCAGCA CTTACTAGCT GACAAAACT TTTCCGTATT

115	1160	1170	1180	1190	1200
CGGAATTAGA	TTTTTATGCA	AGCAATGTTT	CATTTTACA	CAGTATAGTA	TTTATTCTTA
1210	1220	1230	1240	1250	1260
CTTTTGATTA	TATTGCTCGC	ACCCTAAATG	ACAGGTATTA	GAAATTAACC	GCTTTTCAGA
1270	1280	1290	1300	1310	1320
GTATTTTAA	TCTTCTTAGT	ACTAGTTTAG	TTCTTTAAAT	AAGAAACCAT	CTAGTTTTTC
1330	1340	1350	1360	1370	1380
ATTATCACTC	AACTTCAGTC	GGACAAATTT	TAAATTTTTT	ACTCGATAAA	AAAATTTTAT
1390	1400	1410			
AATTCAGACA	AATTATGTCT	TCTCATTTTT	GATCGCT		

1 20 30 40 50 60
 TCATGTTTCA CGGAACGACG AATTTATCCC GTCGTTTCTT CTTTCCGTT TTAACATCA
 70 80 90 100 110 120
 TCTCTTCCTG GATCCTTCAG AGCTCTTGTC AATTCCTCAC GTTTTTTTTT GTTTTTTCGT
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 190 200 210 220 230 240
 CTCCGTGTCC TTCTACTTAC TCTGATTGCC TTAGTTAGTC ACATCGCAAG CAACAATAA
 250 260 270 280 290 300
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 310 320 330 340 350 360
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 430 440 450 460 470 480
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 610 620 630 640 650 660
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 670 680 690 700 710 720
 GCTTCATACA AAAACATTTA ACTAGTGTTT TTCCAGTTTT GTGTTGTTTT CATTTTCTCA
 730 740 750 760 770 780
 CCAAACTGAC AATAATTACT TTCTGTGAAC GTGTTTTGTA GGCAAGCTCC CGAATATTTT
 790 800 810 820 830 840
 TTTCTCTTCT CACGTCTTGT TATTTTCTCG ATTTATTTT CTGAATCTGT GCGGTTTTCA
 850 860 870 880 890 900
 ATCAATTTGA TTGCGATAAT TATTCTATCA GAAATATATT TTCAGAAATC CAAATACTCC
 910 920 930 940 950 960
 AGGTGCCAAT GCGGTGAAAG AAAATTATGA AGTTTATTCC TGAAATCACA CTACTCTTGC
 970 980 990 1000 1010 1020
 TTTTATTTGT AACTCTTACA CAGGTTAGTT GGTTGATTCT AGATCTCTTG CCTCCTAGCT
 1030 1040 1050 1060 1070 1080
 TGCAAGGATA ATATAATTGA ATTGTTTTTG AGGAGTGCAA AGATTGAATA GTTTCTTATA
 1090 1100 1110 1120 1130 1140
 TTTAGGCTAA AGGAAAACGA CGGAAATGTC CGGAGGGTGC GTGGTCGGAA GGAAAGATTA

1150 1160 1170 1180 1190 1200
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 1930 1940 1950 1960 1970 1980
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 1990 2000 2010 2020 2030 2040
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 2050 2060 2070 2080 2090 2100
 CAAACTGGTC CCCTGGGTGG GGAAATGGTG GCATTTTGG AAACATTTTC ATAGTCGAAG
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 AAGTGAACA AGAAAATTGG AAAATAGAGA TACATATGTA TATGAAAATA GAATTGAACA
 2170 2180 2190 2200 2210 2220
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 2230 2240 2250 2260 2270 2280
 ATTGACATTT TATTCATCTA ACTGTGGCAT GACTCGGCAC TTTCTTTTGC TCATCTTCCG

229 2300 2310 2320 2330 2340
 GCTTGTAAGC GGTAAAGAAAT CTTTGTATTA GAAGGGAAAA ATATTTAAAT TAATGAAATT
 2350 2360 2370 2380 2390 2400
 TCAGAAATAT CACAATGGAA ACACGACTTT TACCTAAGAT TTGGTCTCCA AACACGTGTA
 2410 2420 2430 2440 2450 2460
 TGATTAATTC AAAACGAACA ACCGTCCATG CATCACCATC GGAAAATGTG ATGGTTATTC
 2470 2480 2490 2500 2510 2520
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 2530 2540 2550 2560 2570 2580
 TGTAGCAAGA AAAAAACGGA TTCTTGTCTC TGTCGACGTT TCCTAAGTAT TGTGAATTAT
 2590 2600 2610 2620 2630 2640
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 2890 2900 2910 2920 2930 2940
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 2950 2960 2970 2980 2990 3000
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 3010 3020 3030 3040 3050 3060
 CAGAAGAAGT TGAACCTCAT TGGATGGAAG AAGCTGTCAC ATTAATGAAG CCAATTCAAC
 3070 3080 3090 3100 3110 3120
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 3250 3260 3270 3280 3290 3300
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 TCCAGTTTGG AAATATTTTG AAAAATCTTC CAAGGGTTTC ATATGTGAAA GGTTCGTTTT
 3370 3380 3390 3400 3410 3420
 TTTTCTTTTT CAAACAAATA AAAAAAAGA TAAACAAATA TTTGTTTCAG CAATGGATGT

3410 3440 3450 3460 3470 3480
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 3670 3680 3690 3700 3710 3720
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 4390 4400 4410 4420 4430 4440
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 5350 5360 5370 5380 5390 5400
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 5470 5480 5490 5500 5510 5520
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 5530 5540 5550
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1 20 30 40 50 60
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 910 920 930 940 950 960
 GCAATGGATG TGTGGATGCT TGGATGCATA TCATTTGTCT TCGGAACCAT GGTAGAATTG
 970 980 990 1000 1010 1020
 GCATTTGTTT GTTACATTTT CCGTTGTCAG AACAGCGTAA GAAACGCGGA ACGACGACGG
 1030 1040 1050 1060 1070 1080
 GAACGAATGA GAATTTCTCA GGTGTGGGCA AACGGATCGT GTAGAACTAG AAGCAACGGG
 1090 1100 1110 1120 1130 1140
 TATGCAAACG GGGGATCTGT AATCTCACAT TATCATCCAA CAAGCAATGG AAATGGGAAT

1150	1160	1170	1180	1190	1200
AATAATCGAC	ATGATACACC	TCAAGTTACT	GGAAGAGGAT	CACCTTCATCG	AAACGGGCCA
1210	1220	1230	1240	1250	1260
CCATCTCCAT	TAAACCTTCA	AATGACTACA	TTTGATTCCG	AGATCCCTCT	GACTTTTGAT
1270	1280	1290	1300	1310	1320
CAGCTGCCAG	TTCCCATGGA	ATCCGATAGA	CCCCTGATTG	AAGAGATGCG	ATCAACATCA
1330	1340	1350	1360	1370	1380
CCACCTCCAC	CATCTGGATG	TCTGGCCAGA	TTCCATCCGG	AAGCAGTGGA	CAAATTCTCC
1390	1400	1410	1420	1430	1440
ATTGTAGCTT	TTCCATTGGC	ATTTACAATG	TTTAATCTTG	TCTACTGGTG	GCACTATTTG
1450	1460	1470			
TCTCAAACCTT	TCGATCAAAA	CTATCAGTGA			

The MOD-1 Channel is Activated by Serotonin

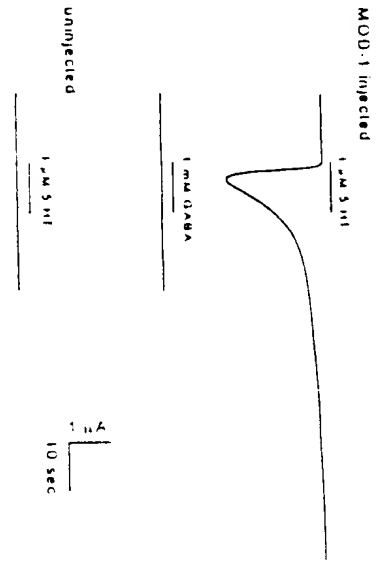


Fig. 9a

Relative Peak Current

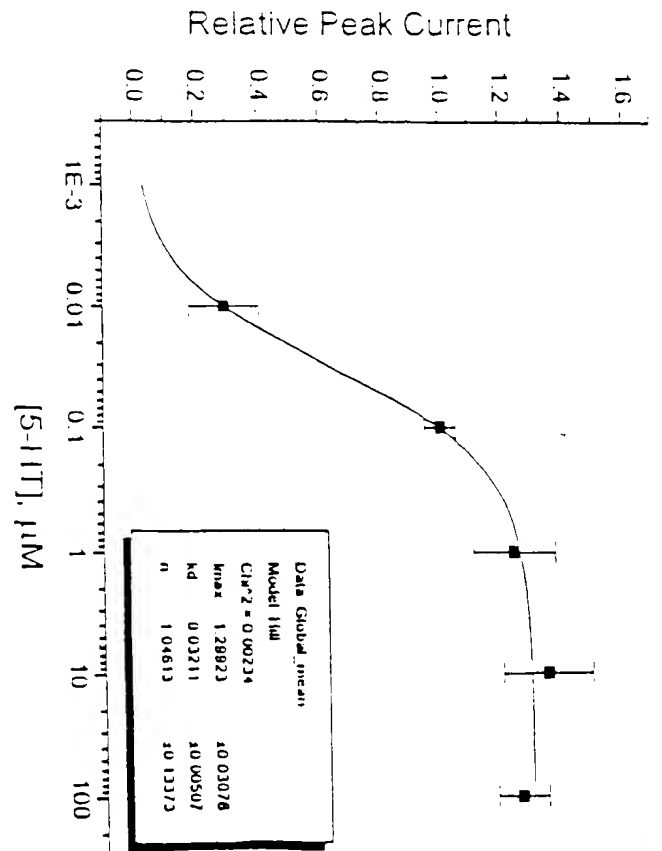


Fig. 9b

Fig. 9c

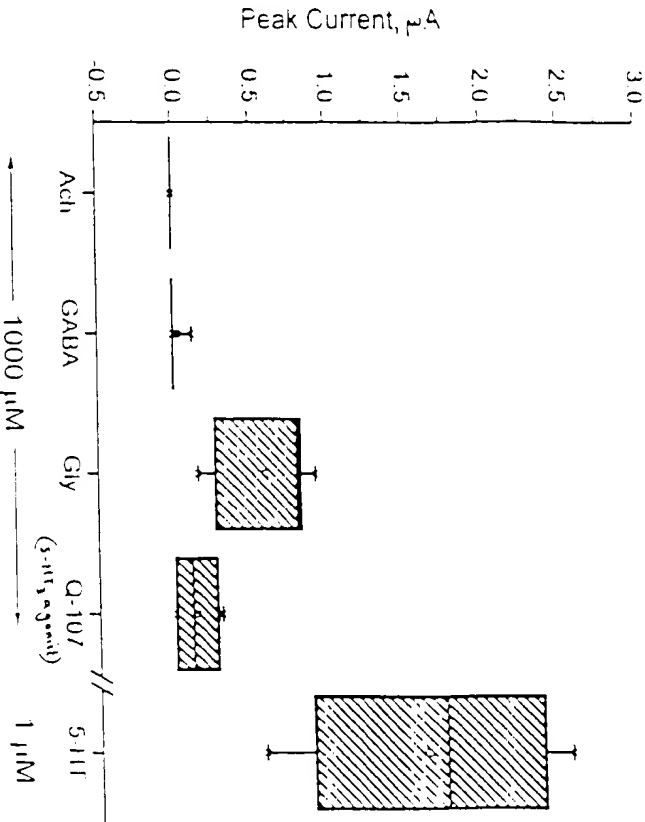


Fig. 9

MOD-1 Selectivity

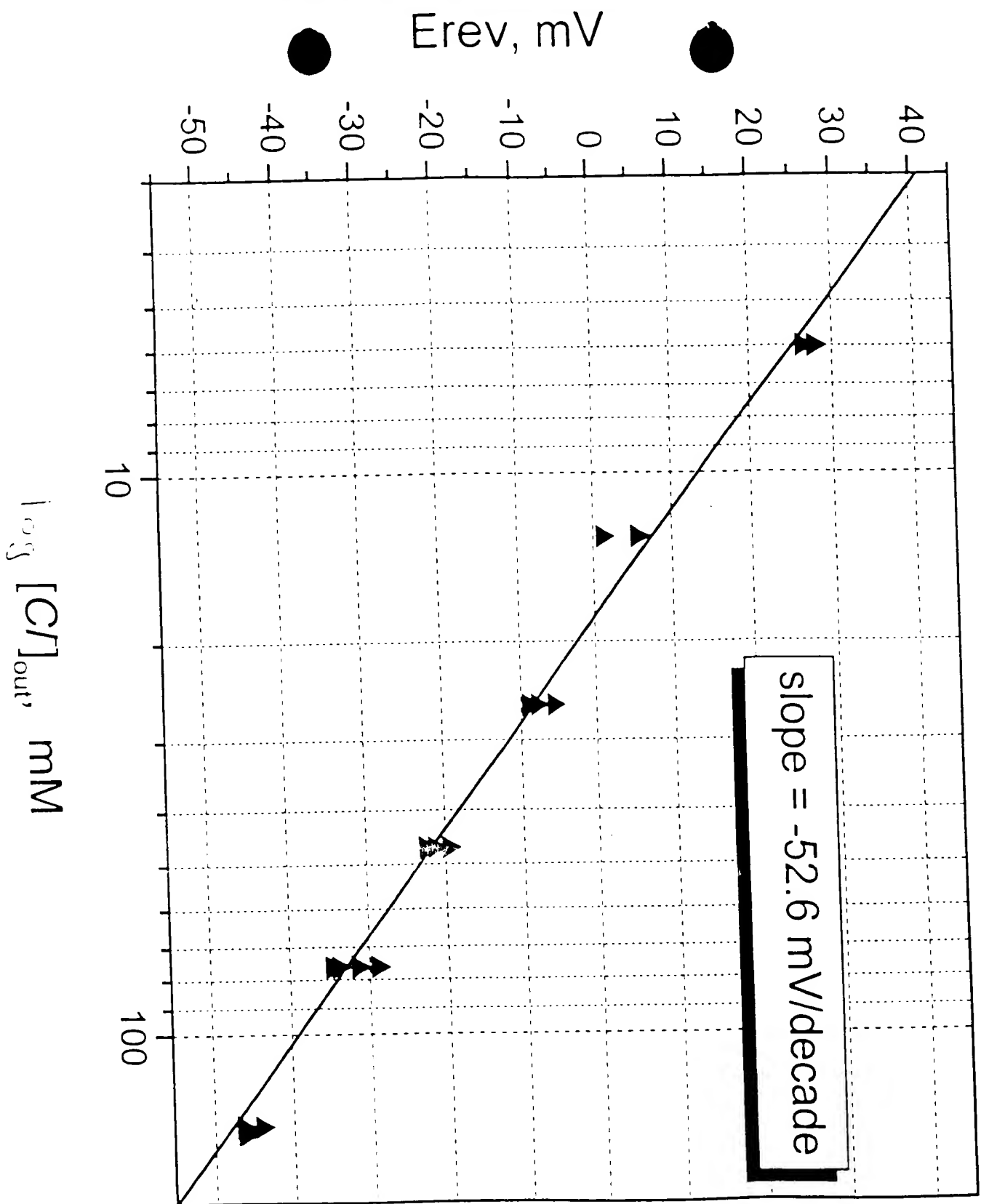
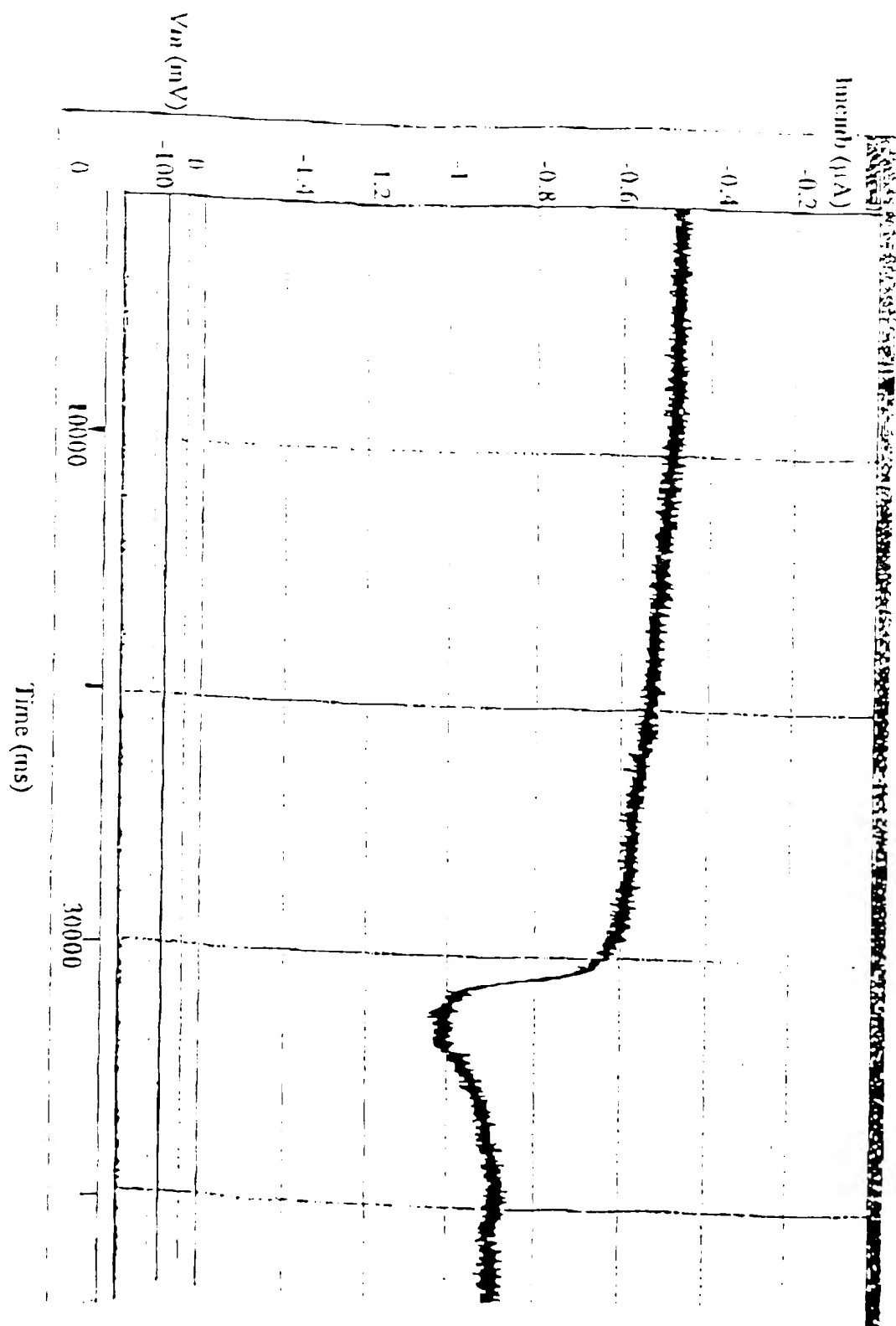


Fig. 10



04/01/2000

Figure 11